

US-09-541-462B-2 (1-108) x AY072430 (1-666)

RESULT 15

LOCUS AY052401, 357 bp mRNA linear PLN 16-OCT-2001

DEFINITION *Arabidopsis thaliana* ring box-1-like protein mRNA, complete cds.

ACCESSION AY052401

VERSION AY052401.1 GI:16186264

KEYWORDS

SOURCE *Arabidopsis thaliana*.

ORGANISM *Arabidopsis thaliana*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 357)

AUTHORS (Okresz, L.)

TITLE Direct Submission

JOURNAL Submitted (25-AUG-2001) Institute of Plant Biology, Biological
Research Center, Temesvari krt. 62, Szeged H-6701, Hungary

FEATURES	Location/Qualifiers
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source      1.  .357
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/db xref="taxon:3702"
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CDS 1.357

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/note="RBX1-2"
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/codon start=1
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BASE COUNT	91 a	83 c	94 g	89 t
ORIGIN				

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Score:	514.50	Matches:	92
Percent Similarity:	83.76%	Conservative:	6
Best Local Similarity:	78.63%	Mismatches:	8
Query Match:	83.52%	Indels:	11
DB:	8	Gaps:	2

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		:: ::	
Db	4	GCGACTCTAGACTCCGACGTTACCATGATTCTCGCCGAGAAGCCTCCAGCAGCGTAGCC	63
Qy	13	---ThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAla	31
		::::: :: :: :: ::	
Db	64	GCGTCGTCTTCCAACAAGAAAGCTAAGCGATTCTGAAATTAAGAAGTGGAGCGCCGTTGCT	123
Qy	32	LeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAsp	51
Db	124	CTCTGGGCTTGGGATATCGTTGTTGACAACTGTGCGATCTGCAGAAACCACATCATGGAT	183
Qy	52	LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla	71
Db	184	CTTTGTATCGAGTGTCAGGCTAATCAGGCCAGTGCCACAAGTGAAGAGTGCAGTGTAGCT	243
Qy	72	TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArg	91
Db	244	TGGGGGGTTTGTCAATCACGCCTTCCACTTTCAGTGCATCAGCAGATGGCTAAAGACTCGT	303
Qy	92	GlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis	108
Db	304	CAAGTTTGTCCATTGGATAACAGTGAGTGGGAGTTTCAGAAATATGGTTCAC	354

GenCore version 5.1.4_p5_4578
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A ROC1

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M A A A M D V D T P S G T N S G A G K K R F E V K K W N A V 30
GCCCTCTGGGCCTGGGATATTGTGGTTGATAACTGTGCCATCTGCAGGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCAG 180
A L W A W D I V V D N C A I C R N H I M D L C I E C Q A N Q 60
CGGTCCGCTACTTCAGAAGAGTGTACTGTGCATGGGGAGTCTGTAACCATGCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACA 270
A S A T S E E C T V A W G V C N H A F H F H C I S R W L K T 90
CGACAGGTGTGTCCATTGGACAACAGAGAGTGGGAATTCCAAAAGTATGGGCACTAG 327
R Q V C P L D N R E W E F Q K Y G H * 108

B ROC2

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GATGCCTGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTTGGTCTGGGGAGAATGTAATCATTCCCTCCACAACTGCTGC 180
D A C L R C Q A E N K Q E D C V V V W G E C N H S F H N C C 60
ATGTCCCTGTGGGTGAAACAGAACAAATCGCTGCCCTCTCTGCCAGCAGGACTGGGTGGTCCAAAGAATCGGCAAATGA 258
M S L W V K Q N N R C P L C Q Q D W V V Q R I G K * 85

C

ROC1-Hs 22 FEVKKWNAVALWAWDIVVDNCAICRNHIMDLCECQANQASATSEECTVAVGWVCNHAFHFHCISRWL---KTRQVCPLDNREWEF 108
ROC1-Dm 22 FEVKKWNAVALWAWDIVVDNCAICRNHIMDLCECQANQASATSEECTVAVGWVCNHAFHFHCISRWL---KTRQVCPLDNREYDF 108
ROC1-Ce 24 FEVKKWSAVALWAWDIQVDNCAICRNHIMDLCECQANQAAGLKDECTVAVGNCNHAFHFHCISRWL---KTRQVCPLDNREWEF 110
ROC1-At 32 FEIKKWSAVALWAWDIVVDNCAICRNHIMDLCECQANQASATSEECTVAVGWVCNHAFHFHCISRWL---KTRQVCPLDNSEWEF 118
ROC1-Sp 21 FEIKKWNAVALWQWDIVVDNCAICRNHIMDLCECQANTDSAAQECTVAVGWTCNHAFHFHCISRWL---NTRNVCPLDNREWEF 113
ROC1-Sc 35 FEIKKWTAVAFWSWDIAVDNCAICRNHIMEPCIECQPKAMTDTDNECVAAGVVCNHAFHLHCINKWI---KTRDACPLDNQPWQL 121
ROC2-Hs 2 FSLKKWNAVAMWSWDVECDTCAICRVQVMDACLRCQAEN---RQEDCVVVWGECNHSFHNCCMSLWV---RQNNRCPLCQQDWV 85
ROC2-Ce 30 FVLKKWNAVALWAWDVECDTCAICRVHLMEECLRCQSEP---SAE-CYVVWGDNCNHSFHCCMTQWI---RQNNRCPLCQKDWV 112
APC11-Hs 3 VKIKCWNGVATWLWVANDENCGICRMAFNGCCPDCKVPG-----DDCPLVWGQCSCFHMHCILKWLHAQQVQQHC PMCRQEWKF 84
APC11-Dm 3 VTIKSWTGVATWRWIANDENCGICRMSFESTCPECALPG-----DDCPLVWGVCSHCFHMHCIVKWLNLQPLNKQC PMCRQSWKF 85
APC11-Ce 51 ITVKKLHVCGEWKWL[3]DTCGICRMEFESACNMCKFPG-----DDCPLVLGICRHAFHRHCIDKWI[5]QPRACPLCRQDWTI 135
APC11-Sc 3 VKINEVHSVFAWSW[21]DVCGICRASYNCTPSCKFPG-----DQCPLVIGLCHHNFHDHC IYRWLDTPTSKGLC PMCRQTFQL 165

FQKYGH"
 BASE COUNT 85 a 75 c 94 g 73 t
 ORIGIN

Query Match 100.0%; Score 327; DB 9; Length 327;
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 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    181 GCGTCCGCTACTTCAGAAGAGTGTACTGTTCGCATGGGGAGTCTGTAACCATGCTTTTCAC 240
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Qy    241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAACAGAGAG 300
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Db    301 TGGGAATTCCAAAAGTATGGGCACTAG 327
  
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RESULT 2

AF140598

LOCUS AF140598 508 bp mRNA linear PRI 11-MAY-1999

DEFINITION Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.

ACCESSION AF140598

VERSION AF140598.1 GI:4769003

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 508)

AUTHORS Kamura,T., Koepp,D.M., Conrad,M.N., Skowrya,D., Moreland,R.J.,
Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Elledge,S.J.,
Conaway,R.C., Harper,J.W. and Conaway,J.W.

TITLE Rbx1, a component of the VHL tumor suppressor complex and SCF
 ubiquitin ligase

JOURNAL Science 284(5414), 657-661 (1999)

MEDLINE 99234320

PUBMED 10213691

REFERENCE 2 (bases 1 to 508)

AUTHORS Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.

TITLE Direct Submission

JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma

